

SEQUENCE LISTING

<110> Shyjan, Andrew W.

<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
AND TREATMENT OF TUMOR PROGRESSION

<130> 07334/004005

<140> US 09/181,030

<141> 1998-10-27

<150> US 08/862,442

<151> 1997-05-23

<150> US 08/623,679

<151> 1996-03-29

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ctaacagatg ttgtgtgtgt cagctacta accagcacat cccccccttg ccgagtgggg	180	
ctcccgacac aacaggagag gacaccaagc aggcagacac gcagtcggg aaatggctcg	240	
tcagcaaaca caccagagc taccacacag actcctatgg gattcttcaa ttccagggtg	300	
ggggttactc caataaaagcc atg tac atc cga gtc tcc tac gac acc aag cca	353	
Met Tyr Ile Arg Val Ser Tyr Asp Thr Lys Pro		
1	5	10

gat tcc ctg ctc cac ctc atg gtg aag gac tgg cag ctg gag ctc ccg	401	
Asp Ser Leu Leu His Leu Met Val Lys Asp Trp Gln Leu Glu Leu Pro		
15	20	25

aag ctc ttg ata tct gtg cac gga ggc ctc caa agc ttc gag atg cag Lys Leu Leu Ile Ser Val His Gly Gly Leu Gln Ser Phe Glu Met Gln 30 35 40	449
tcc aaa ctg aag cag gtg ttt ggg aaa ggt ctg atc aag gct gcc atg Ser Lys Leu Lys Gln Val Phe Gly Lys Gly Leu Ile Lys Ala Ala Met 45 50 55	497
acc acg ggg gcg tgg atc ttc acc ggg ggt gtg agc act ggt gtc gtc Thr Thr Gly Ala Trp Ile Phe Thr Gly Gly Val Ser Thr Gly Val Val 60 65 70 75	545
agc cat gtg ggg gat gcc ttg aaa gac cac tcc tcc aag tcc aga ggc Ser His Val Gly Asp Ala Leu Lys Asp His Ser Ser Lys Ser Arg Gly 80 85 90	593
cgg ctc tgt gct ata gga att gct ccc tgg ggc atg gtg gag aac aag Arg Leu Cys Ala Ile Gly Ile Ala Pro Trp Gly Met Val Glu Asn Lys 95 100 105	641
gaa gac ctg att gga aaa gat gta aca aga gtc tat cag acc atg tcc Glu Asp Leu Ile Gly Lys Asp Val Thr Arg Val Tyr Gln Thr Met Ser 110 115 120	689
aac cct ctg agc aag ctc tct gtg ctc aac aat tcc cac act cac ttc Asn Pro Leu Ser Lys Leu Ser Val Leu Asn Asn Ser His Thr His Phe 125 130 135	737
atc ttg gct gac aac ggc acc ctg ggc aag tat ggt gct gag gtg aag Ile Leu Ala Asp Asn Gly Thr Leu Gly Lys Tyr Gly Ala Glu Val Lys 140 145 150 155	785
ctt cga aga cag ctg gaa aaa cac atc tcc ctg cag aag atc aac aca Leu Arg Arg Gln Leu Glu Lys His Ile Ser Leu Gln Lys Ile Asn Thr 160 165 170	833
agg ctg ggc cag ggt gta cct gtc gtg ggc cta gtg gta gaa ggt ggt Arg Leu Gly Gln Gly Val Pro Val Val Gly Leu Val Val Glu Gly Gly 175 180 185	881
cct aac gtg gtt tct atc gtc ctg gag tat ctc aaa gaa gac cct cct Pro Asn Val Val Ser Ile Val Leu Glu Tyr Leu Lys Glu Asp Pro Pro 190 195 200	929
gtc cct gtg gtg gtt tgc gat ggc agt gga cgt gcc tct gac att ttg Val Pro Val Val Cys Asp Gly Ser Gly Arg Ala Ser Asp Ile Leu 205 210 215	977
tcc ttc gca cac aaa tac tgc gac gaa gga gga gtc ata aac gag tcc Ser Phe Ala His Lys Tyr Cys Asp Glu Gly Gly Val Ile Asn Glu Ser 220 225 230 235	1025
ctg cgg gac cag ctt cta gtt acc att cag aaa aca ttt aat tac agc Leu Arg Asp Gln Leu Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser 240 245 250	1073
aag tcc cag tcg tat cag ctg ttt gca att atc atg gag tgc atg aag Lys Ser Gln Ser Tyr Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys 255 260 265	1121

aag aaa gaa ctc gtc act gtg ttt cgg atg ggt tcc gag ggt cag caa Lys Lys Leu Val Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln 270 275 280	1169
gat gtc gag atg gca att tta act gcc ttg ctc aaa gga acc aac gca Asp Val Glu Met Ala Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala 285 290 295	1217
tca gct cca gat cag ctg agc ttg gcc ctg gct tgg aac cgg gtc gac Ser Ala Pro Asp Gln Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp 300 305 310 315	1265
ata gcg cga agc cag atc ttc gtc ttt ggc cca cac tgg ccc cca ctg Ile Ala Arg Ser Gln Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu 320 325 330	1313
gga agc ctg gcc cct cct gtg gac acc aaa gcc gca gag aag gaa aag Gly Ser Leu Ala Pro Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys 335 340 345	1361
aag cca ccc aca gcc acc acc aag ggg aga gga aaa gga aaa ggc aag Lys Pro Pro Thr Ala Thr Thr Lys Gly Arg Gly Lys Gly Lys Gly Lys 350 355 360	1409
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gat gct ctt gtc cta gat cgg gtg gac ttt gta aag ctc ctg att gaa Asp Ala Leu Val Leu Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu 400 405 410	1553
aac gga gtg aac atg cag cat ttc ctc acc atc ccg agg ctg gag gag Asn Gly Val Asn Met Gln His Phe Leu Thr Ile Pro Arg Leu Glu Glu 415 420 425	1601
cta tac aac acc aga ctg ggc cca cca aac acc ctt cat ctg ctg gtg Leu Tyr Asn Thr Arg Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val 430 435 440	1649
cgg gat gta aag aag agc aac ctt cca cct gat tac cac atc agc ctc Arg Asp Val Lys Lys Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu 445 450 455	1697
att gat ata gga ctg gtg ctg gag tac ctc atg ggc ggt gcc tac cgc Ile Asp Ile Gly Leu Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg 460 465 470 475	1745
tgc aac tac act cgg aaa agc ttc cgg act ctc tac aac aac ttg ttt Cys Asn Tyr Thr Arg Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe 480 485 490	1793
ggc cct aag agg gta gag ctc agc aga cac aca gtg tcc tgt gcc tcc Gly Pro Lys Arg Val Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser 495 500 505	1841

cag agt aac atg tgg ttc ctt gat gtg ctt ccc caa aag ccc acc tgt Gln Ser Asn Met Trp Phe Leu Asp Val Leu Pro Gln Lys Pro Thr Cys 510 515 520	1889
gca gaa tgc aac tct tca cct cac ctg tcc caa act gac atc acc cca Ala Glu Cys Asn Ser Ser Pro His Leu Ser Gln Thr Asp Ile Thr Pro 525 530 535	1937
cct ctg ccc tgacacccag tgcagggcct cctagcttc acatgcagcc Pro Leu Pro 540	1986
attcacatcg cctctcaaga ctggccagg cagtgcacc tgcggccat gtctgtcc ccctccttcc tacaatagcc cccccctctgg gccccatgcc tctgcctct cagcccgttc tcttccac tgatcaactgg cgctccgtt gtcttccaag gcaagaaaca aggaaaagca tcttttgc cacaaaaagtt tagggctccc cgctgttcaa ccatagccaa cctcaactgt catcgagtc atccaggcca gctgccacac acaaggcttc cccacccat cccaaatagac cctattcctc catcaaaatc aaagctaact cctggcctgc cacattgctt cttcttgctc cagcctgtta aacctccaat aaatgtcaga tctgtggaa gccttcctca ctctcactcc acagtttgc aagagagcga gaggctcggt tggttctact tacaaggaag gctttgtgtc tgtctgtcct tcccaactga cttctgtga cagaagcagt ttccacatga aagcggttgc tcacctggat gttgtcatta attaataatgt atacaaaaata ttgacacttc ttttcctgt tctttgttat gcaagccgaaa gcaacttaagc ttctggaaat ggaagtaagt aggacatgtt tgtggcagtt tatttactat atataccctt gtcattctgt ggaagcaaaa attgcaatgt tttccatgaa taaaagctcggt gcc	2046 2106 2166 2226 2286 2346 2406 2466 2526 2586 2646 2706 2729
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Leu Val Thr Ile Gln Lys Thr Phe Asn Tyr Ser Lys Ser Gln Ser Tyr
 245 250 255
 Gln Leu Phe Ala Ile Ile Met Glu Cys Met Lys Lys Lys Glu Leu Val
 260 265 270
 Thr Val Phe Arg Met Gly Ser Glu Gly Gln Gln Asp Val Glu Met Ala
 275 280 285
 Ile Leu Thr Ala Leu Leu Lys Gly Thr Asn Ala Ser Ala Pro Asp Gln
 290 295 300
 Leu Ser Leu Ala Leu Ala Trp Asn Arg Val Asp Ile Ala Arg Ser Gln
 305 310 315 320
 Ile Phe Val Phe Gly Pro His Trp Pro Pro Leu Gly Ser Leu Ala Pro
 325 330 335
 Pro Val Asp Thr Lys Ala Ala Glu Lys Glu Lys Lys Pro Pro Thr Ala
 340 345 350
 Thr Thr Lys Gly Arg Gly Lys Gly Lys Lys Lys Gly Lys Val
 355 360 365
 Lys Glu Val Glu Glu Thr Asp Pro Arg Lys Leu Glu Leu Leu
 370 375 380
 Asn Trp Val Asn Ala Leu Glu Gln Ala Met Leu Asp Ala Leu Val Leu
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 Asp Arg Val Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met
 405 410 415
 Gln His Phe Leu Thr Ile Pro Arg Leu Glu Leu Tyr Asn Thr Arg
 420 425 430
 Leu Gly Pro Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys
 435 440 445
 Ser Asn Leu Pro Pro Asp Tyr His Ile Ser Leu Ile Asp Ile Gly Leu
 450 455 460
 Val Leu Glu Tyr Leu Met Gly Gly Ala Tyr Arg Cys Asn Tyr Thr Arg
 465 470 475 480
 Lys Ser Phe Arg Thr Leu Tyr Asn Asn Leu Phe Gly Pro Lys Arg Val
 485 490 495
 Glu Leu Ser Arg His Thr Val Ser Cys Ala Ser Gln Ser Asn Met Trp
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23

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gagactcagc	ctgagaaatg	gtctgtgcc	aagcacaccc	agagctaccc	aacagattcc	300
tatggagttc	ttgaattcca	gggtggcgg	tattccaata	aagcc	atg tat atc cgt	357
Met Tyr Ile Arg						
1						
gta tcc tat	gac acc aag	cca gac tca	ctg ctc cat	ctc atg	gtg aaa	405
Val Ser Tyr	Asp Thr Lys	Pro Asp Ser	Leu Leu His	Leu Met Val	Lys	
5	10	15	20	25	30	35
gat tgg cag	ctg gaa ctc	ccc aag ctc	tta ata tct	gtg cat	gga ggc	453
Asp Trp Gln	Leu Glu Leu	Pro Lys Leu	Leu Ile Ser	Val His	Gly Gly	
25	30	35	40	45	50	501
ctc cag aac	ttt gag atg	cag ccc aag	ctg aaa caa	gtc ttt	ggg aaa	549
Leu Gln Asn	Phe Glu Met	Gln Pro Lys	Leu Lys Gln	Val Phe	Gly Lys	
40	45	50	55	60	65	597
ggc ctg atc	aag gct atg	acc acc ggg	gcc tgg atc	tcc acc	ggg	645
Gly Leu Ile	Lys Ala Ala	Met Thr	Gly Ala Trp	Ile Phe	Thr Gly	
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ggt gtc agc	aca ggt gtt	atc agc cac	gta ggg	gat gcc	ttg aaa gac	789
Gly Val Ser	Thr Gly Val	Ile Ser His	Val Gly Asp	Ala Leu	Lys Asp	
70	75	80	85	90	95	100
cac tcc tcc	aag tcc aga	ggc cgg	gtt tgt	gct ata	gga att	693
His Ser Ser	Lys Ser Arg	Gly Arg Val	Cys Ala Ile	Gly Ile	Ala Pro	
85	90	95	100	105	110	115
tgg ggc atc	gtg gag aat	aag gaa gac	ctg gtt	gga aag	gat gta aca	837
Trp Gly Ile	Val Glu Asn	Lys Glu Asp	Leu Val	Gly Lys	Asp Val Thr	
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aga gtg tac	cag acc atg	tcc aac cct	cta agt aag	ctc tct	gtg ctc	885
Arg Val Tyr	Gln Thr Met	Ser Asn Pro	Leu Ser Lys	Leu Ser Val	Leu	
120	125	130	135	140	145	170
aac aac tcc	cac acc cac	ttc atc	ctg gct	gac aat	ggc acc	885
Asn Asn Ser	His Thr His	Phe Ile Leu	Ala Asp Asn	Gly Thr	Leu Gly	
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tcc ctc cag	aag atc aac	aca aga	ctg ggg	cag ggc	gtg ccc	180
Ser Leu Gln	Lys Ile Asn	Thr Arg Leu	Gly Gln	Gly Val	Pro Leu Val	
165	170	175	180	185	190	195

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cag aaa aca ttt aat tat aat aag gca caa tca cat cag ctg ttt gca Gln Lys Thr Phe Asn Tyr Asn Lys Ala Gln Ser His Gln Leu Phe Ala 245 250 255 260	1125
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aaa gcc acg gag aag gag aag cca ccc atg gcc acc acc aag gga Lys Ala Thr Glu Lys Glu Lys Pro Pro Met Ala Thr Thr Lys Gly 345 350 355	1413
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gac ttt gtg aag ctc ctg att gaa aac gga gtg aac atg caa cac ttt Asp Phe Val Lys Leu Leu Ile Glu Asn Gly Val Asn Met Gln His Phe 405 410 415 420	1605

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cca aac aca ctt cat ctg ctg gtg agg gat gtg aaa aag agc aac ctt Pro Asn Thr Leu His Leu Leu Val Arg Asp Val Lys Lys Ser Asn Leu 440 445 450	1701
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ggg gaa gag agc atg gcc aag gcc ctg gtg gcc tgc aag ctc tac aag Gly Glu Ser Met Ala Lys Ala Leu Val Ala Cys Lys Leu Tyr Lys 565 570 575 580	2085
gcc atg gcc cac gag tcc tcc gag agt gat ctg gtg gat gac atc tcc Ala Met Ala His Glu Ser Ser Glu Ser Asp Leu Val Asp Asp Ile Ser 585 590 595	2133
cag gac ttg gat aac aat tcc aaa gac ttc ggc cag ctt gct ttg gag Gln Asp Leu Asp Asn Asn Ser Lys Asp Phe Gly Gln Leu Ala Leu Glu 600 605 610	2181
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ccc ggc ctg aag gtt atc atg ggg att ctt cta ccc ccc acc atc ttg Pro Gly Leu Lys Val Ile Met Gly Ile Leu Leu Pro Pro Thr Ile Leu 680 685 690	2421
ttt ttg gaa ttt cgc aca tat gat gat ttc tcg tat caa aca tcc aag Phe Leu Glu Phe Arg Thr Tyr Asp Asp Phe Ser Tyr Gln Thr Ser Lys 695 700 705	2469
gaa aac gag gat ggc aaa gaa aaa gaa gag gaa aat acg gat gca aat Glu Asn Glu Asp Gly Lys Glu Lys Glu Asn Thr Asp Ala Asn 710 715 720	2517
gca gat gct ggc tca aga aag ggg gat qag qag aac gag cat aaa aaa Ala Asp Ala Gly Ser Arg Lys Gly Asp Glu Glu Asn Glu His Lys Lys 725 730 735 740	2565
cag aga att atc ccc atc gga aca aaa atc tgt aaa ttc tat aac gcg Gln Arg Ile Ile Pro Ile Gly Thr Lys Ile Cys Lys Phe Tyr Asn Ala 745 750 755	2613
ccc att gtc aag ttc tgg ttt tac aca ata tca tac ttg ggc tac ctg Pro Ile Val Lys Phe Trp Phe Tyr Thr Ile Ser Tyr Leu Gly Tyr Leu 760 765 770	2661
ctg ctg ttt aac tac gtc atc ctg gtg cg ^g atg gat ggc tgg ccg tcc Leu Leu Phe Asn Tyr Val Ile Leu Val Arg Met Asp Gly Trp Pro Ser 775 780 785	2709
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gtc gtg ctc atg agt ttc gga gta gcc cgt caa gcc att ctg cat cca Val Val Leu Met Ser Phe Gly Val Ala Arg Gln Ala Ile Leu His Pro 870 875 880	2997
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gcc atg gaa att aat cct cct tgt ggt gag aac cta tat gat gag gag Ala Met Glu Ile Asn Pro Pro Cys Gly Glu Asn Leu Tyr Asp Glu Glu 920	925	930	3141	
ggc aag cgg ctt cct ccc tgt atc ccc ggc gcc tgg ctc act cca gca Gly Lys Arg Leu Pro Pro Cys Ile Pro Gly Ala Trp Leu Thr Pro Ala 935	940	945	3189	
ctc atg gcg tgc tat cta ctg gtc gcc aac atc ctg ctg gtg aac ctg Leu Met Ala Cys Tyr Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu 950	955	960	3237	
ctg att gct gtg ttc aac aat acc ttc ttt gaa gta aaa tca ata tcc Leu Ile Ala Val Phe Asn Asn Thr Phe Phe Glu Val Lys Ser Ile Ser 965	970	975	980	3285
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